Page 1 of 7



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RAW SEQUENCE LISTING

FATENT APPLICATION: US/09/673,166A

- PATE: 12/26/23/02 - TIME: 13:34:57

Input Set : A:\19624051.app

Output Set: N:\CRF4\12262002\1673166A.raw

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116% AFFLICANT: Le Gal, Frédérique Anne
         Filler, Jean Gerard
         Jahery-Segard, Hanne
         Gras-Masse, Helene
        Melnyk, Oleg
         Tartar, Amdre
16 ×12c> Tible of invention: Lifofeffides immiding t lymphodyfic dytotoxidity
        BEARING AT LEAST ONE AUXILIARY T EPITOFE, AND USES FOR
         VACCINATION
14 :13(> FILE REFERENCE: 102.174
    140 → CURRENT APPLACATION NUMBER: 09/673,166A
1 6
17 < 141 > CUFRENT FILING DATE: 2001-04-04
19 kise Frior Afflication NUMBER: FCT/Fk99/06792
20 Plain PRIOR FILING DATE: 1999-04-00
12 RIGG: NUMBER OF SEQ ID NOS: 276
24 <1785 SOFTWARE: Fatentin Ver. 2.1
26 K210% BEG ID NO: 1
20 ×211 · LENGTH: 14
18 MINE TYPE: FRT
   22135 ORGANISM: Clostridium tetanus
31 KARCH FEATURE:
   (2P3) OTHER INFORMATION: amino acids 830-843 of the tetanus toxif.
34 <400 > SEQUENCE: 1
35 Gin Tyr Ile Lys Ala Ash Ser Lys Phe Ile Gly He Thr Glu
3 (5)
33 stiff from in Mo: W
40 kA11 - LENGTE: 14
41 QUINTYIE: FRI
40 <213 CRGANISM: Human Parillomavirus (HFV)
44 -227% FRATURE:
48 WINE COMPACTOR: mine wide 43-50 they by postein
47 8400 SEPTEMBER &
4r Bly Bin Ala Bin Fro Asy Ard Ala His Ash ile Val Thr Fre
POR ALIMA SERVICE NO. 11 : 3
PARALIZA LENGTH: LA
*4 *.1. * TYEF: ERT
to Eller Of WANTON: Attiticial Compense
** - PLIE NAME REY: 11FII
arrant Williams
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LATE: lavaeralla

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FATENT AFFILMATION: US/09/673,166A TIME: 13:30:31
                Inch: .'-: : A:\19624051.app
                Street: N:\CRF4\12262002\1673166A.raw
\mathcal{R}_{\mathcal{F}} be for the Tyr Lie Lye Ala Asn Der Lye Fhe 110 Thy The Thr Flu
€ 4
ée Ala Aka Ala Ala Ala tiy Ilo Giy ilo box Thr Val
\epsilon 7
70 IND FEG ID NO: 4
Mi Wille I BINGTH: Ar
72 Zize TYPE: PRT
73 - 2157 GRGANISM: Artiffdiai Sequence
U5 2205 FRATURE:
76 - 7217 NAMEZKEY: LIFT
"/ .... ECTATION: (1)
78 | 1252 OTHER INFORMATION: dipaimitoyl-lysyl chaif on N-terminal residue
80 4400> SEQUENCE: 4
81 Cer Sor Gln Tyr Ile Lys Ala Ash Sor Lys Phe Ile Giy Ile Thr Glu
   1
64 Arg Gly Arg Ala Ala Gly Ile Gly Ile Leu Thr Val
   2.0
48 <210> SEÇ ID NO: 5
e9 <211≥ HENGTH: 28
90 :212: TYPE: PRT
91 <213% ORGANISM: Artificial Sequence
93 W220s FEATURE:
94 - 221 NAME/KEY: LIPID
95 <222 LOCATION: (1)
96 <223 OTHER INFORMATION: dipalmitoyl-lysyl chain on N-terminal residue
98 34605 SEQUENCE: 5
99 Gly Arg Gln Tyr lie Lys Ala Ash Ser Lys the Tle Gly lie Thr Gla
* 75,15
10% And Gly Arg Ala Ala Gly II+ Gly In- Ieu Thr Val
     20
103
106 <2.10≥ SEQ ID NO: 6
107 k2115 LENGTH: 28
108 WILLS TYPE: PRT
109 - Viss ORGANISM: Artificial Dequence
III WZCA FEATURE:
110 -711> NAMEZKEY: LIFID
115 % N/2> LOCATION: (1)
114 ×723> OTHER INFORMATION: monopalmitoyi-lysyl chain on N-terminal residue
III. 44000 BEÇUENDE: 6
117 Censer Air Tyr ile lys Ala Asr Gen lys Ene lie My lle ThroMu
La Ang Ray Ara Ala Ala Riy Ile Riy Ile Lea Tha Val
1.4 +.17 + FF, 17 NC:
1.7 +.11 + FFN FFE: .#
lok (11. ) TYPE: PRT
L'OKTION BUANTOY: Antiritie, Composite
. * - I. * FFATTHE:
130 Bulle NAME FEY: 11111
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DATE: 1572k71012

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FATENT APPLICATION: US/09/673,166A
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                ing it. Care: A:\19624051.app
                output Set: N:\CRF4\12262002\1673166A.raw
131 - .... 7 12 2011 2011
151 collections in the MATION: recoverable violates of chain on Newerminal Pasions
134 84162 JRJUEN 18: 0
let Gly Ary Gin Tyr lie Lys Ala Ash Cer Lys The lie Gly lie Thr Glu
13€
198 Ary Sly Arg Ala Ala Sly 11e Sly 11e bed Thr Va.
139
                2.
142 <210> CEQ ID NO: -
143 < 2115 LENGTH: 10
144 F2182 TYPE: PRT
14% #813% (OKSANISM: Artificial Dequations
14V * Pada FRATURE:
148 <223 OTHER INFORMATION: A hydrazine is bound between the N-terminal lysine
149 and isoleucine at position 2
151 <400> SEQUENCE: 8
150 Lys lie Leu Lys Glu Frc Vai His Gly Val
153 1
156 <1.10> SEQ ID NO: 9
187 WARL LENGTH: 11
15% - 212> TYPE: FRT
159 (213) ORGANISM: Artificial Sequence
161 - 220> FEATURE:
162 - 223> OTHER INFORMATION: aldehyde group bound to N- terminal residue
164 <20> FÉATURE:
165 <221: NAME/KEY: LIPID
166 <222> LOCATION: (15)
167 $728 OTHER INFORMATION: palmittyl chain on C-terminal lysine residue
169 <400 SEQUENCE: 9
170 Arg Thr Fre Fre Ala Tyr Arg Fre Fre Ash Ala Ene lle Leu Lys
                                    10
174 <210≥ SEQ ID NO: 10
175 <211> LENGTH: 9
176 <212> TYPE: PRT
177 ×213> ORGANISM: Hemo supions
174 4770 FEATURE:
180 %A23% OTHER INFORMATION: epitope from BCK-ABL fusion protein (chrenic
    myeloid leukemia translöcation)
193 <400> SEQUENCE: 10
194 Glu Asp Ala Glu Leu Ash Fri Ari Fhe
188 - LIP - OF, ID NO: 11
189 - IIIN DENATH: 4
IMPOUNTED TYPE: FRT
191 - VIII - FCANIOM: E.m. sapieno
1 ** * 1.7 * FFATURE:
44 - A - CTHER INF EMATION: 43 h 43 m t F F-AH, inwich 31 tein - Similio
lekoro — myeldia levkemia translogati n
lekoe45 - Begyenyen li
le Ger Na Lea Asp Lea Na Lyk Ny Lea
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- DATE: 12/2//2 52

PATENT APPLICATION: US/09/673,166A - TIME: 13:3 :-3 Ingut Cet : A:\19624051.app ... put 341: N:\CRF4\12262002\1673166A.raw ું હતા ત 2:2 /11 · 2E, 12 1%: 17 and -211 - LEMGTH: 9 LO4 MAIN TYPE: PRI 105 - 2130 ORGANISM: Home sapions 207 - 224 → FEATURE: 208 KALIBA STHER INFORMATION: exitoral from BCB-ABL fusion protein (Shronic mweloid leukemia translocation) Ill 44000 SEQUENCE: 12 712 Amp Gli Leu Glu Ala Val Ero Ann 114 The Kildy SEQ ID NO: 15 217 <1.11 - LENGTH: 9 218 <212> TYPE: PRT 219 <213> ORGANISM: Homo samions 221 <220> FEATURE: 222 < 223> OTHER INFORMATION: eritope from BCR-ABL fusion protein (chronic myeloid leukemia translocation) nns <400> sequence: 13 526 Bys Gli Asp Ala Leu Gln Arg Fro Val 227 1 231 <2.113 LENGTH: 9 232 K2125 TYPE: FRT 233 <2135 ORGANISM: Homo sariens 235 RANCE FEATURE: .36 (213) OTHER INFORMATION: epitope from BCB-ARL fusion protein (chronic 2.37 myeloid leukomia transiccation) 239 -400: PEQUENCE: 14 340 Glu Asy Ala Leu Gln Arg Fro Val Ala 241 1 244 <2105 SEQ ID NO: 15 245 <2115 LENGTH: 9 246 -210> TYPE: FRT 247 8213 > QRGANIGM: Home sapiets 249 -220 FEATURE: 210 + 2235 OTHER INFORMATION: Opition with HCB-ABL fusion protein without myeloid leukemia translecation) 293 k40% SEQUENCE: 18 154 Gly @ld Lys Lou Arr Val Let Gly Lyr Lin will in SEC ID NO: In Distriction ENGITE: M . C KILZ TYPE: FFT Chica Do Shamiam: Hombus plans LAGGELT & MEATURES: 194 Solve Other Informations applying to bor-arm that he provides the contraction of the contractions and the contraction of th nyeloli leskemia transi tati n

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- 1 ATE: 11/1///2:52 FATENT APPLICATION: US/09/673,166A - 11ME: 19:3 :34

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The No Asp The Met His Dail And Blu Fibe
2, 1, 2
202 x218 x 789 in 10: 15
_13 KOTI - NENWTH: →
 .74 - 2125 TYPE: BRT
176 - 1132 OFGANISM: Homo saylens
277 - 3200 FEATURE:
276 - 2232 DOHER INFORMATION: epitope from BOB-ABI, tusion protein (chronic
279 myeldid leukemia transl0 matich)
281 * 40 > SEQUENCE: 17
182 Met Gla Tyr Leu Gli Lys Lys Ash the
2. ** *
286 42105 SEQ ID NG: 18
257 <211> LENGTH: 9
288 KI12 - TYPE: PRT
289 KI13> DRGANISM: Homo sariens
291 <220> FEATURE:
292 <223% OTHER INFORMATION: epitope from BCB-ABL fasion protein (chronic
293
         myeloid leukemia transloration;
295 4400% SEQUENCE: 18
296 Ash Oli Slu Ala Ala Asp Glu Val Phé
297 1
300 <210= 3EQ ID NO: 19
301 <211 LENGTH: 9
302 <212: TYPE: PRT
303 <213> ORGANISM: Homo sapiens
305 ×22C: FEATURE:
306 (773) OTHER INFORMATION: epitopo from BCK-ABL fusion protein (chronic
myeloid leukemia translecation)
309 <400> SEQUENCE: 19
310 Val Asn Gln Glu Arg Phe Arg Met Ile
311 1
314 <216> SEQ ID NO: 20
315 KHIT'S LENGTH: 9
316 CALLY TYPE: PRT
317 kD130 ORGANISM: Homo sapiens
319 W220% FEATURE:
320 K2235 OTHER INFORMATION: epitope from BCR-ABL tusion protein (chronic
         myeldid leukemia translovation)
823 RATES BEQUENCE: 20
374 Law The Win Lys Lew Alaster Win Lew
SJA KAIJAN SEQ IR NO: DI
BIA SZIIS DENGTH: 4
·· · · LL · TYPE: PAT
ssi kulis saks<mark>vanični.</mark> Here sapisna
··· will a menument
to 4 of 18 of THES INPOPMATION: Spirips in model #-ABL institute to the continuing
     nyelviš læskemia transli sati n
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VERIFICATION SUMMARYTATE: 1.728/2017PATENT ARRUNATION: US/09/673,166ATIME: 1::60:34

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Vot; ut Vet: N:\CRF4\12262002\1673166A.raw